EXHIBIT A

>Thursday, April 28, 2005
>DNA92234 [Full]
>887 Sites [All Sites]
>
>   [DNA92234], sheldens
> Lib309
>Sequence confirmed by phredphrap

```
                                          thaI
                                nlaIII    snaBI
                           sphI  fnuDII/mvnI               nnlI
                           nspHI betUI taiI                taqI
                    taiI  nspI  bsh1236I                   xhoI
                    maeII/hpyCH4IV bslWI/splI       tsp509I[M.ecoRI-]
              aluI  hinlI/acyI cac8I  bsaAI         ecoRI  tliI
        sapI  ahaII/bsaHI mluI rsaI                 hpy188I smlI
tsp45I  mboII  aatII  cac8I aflIII maeII/hpyCH4IV   paeR7I        hpy188I aciI
maeIII  hphI  sfoI  earI/ksp632I hpy99I hpyCH4V csp6I aluI apoI  avaI[M.taqI-] mnlI fnu4HI/bsoFI hpy18   bpmI/g
                                                                                        ^insert starts here
1 TAGGTGACAC TATAGAAGAG CTATGACGTC GCATGACACGC GTACGTAAGC TCGGAATTCG GCTCGAGGAA TGAATACCTC CGAAGCCGCT TTGTTCTCCA
  ATCCACTGYG ATATCTTCTC GATACTGCAG CGTACGTNCG CATGCAATTCG AGCCTTAAGC CGAGCTCCTT ACTTATGGAG GCTTCGGGCGA AACAAGAGGT
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GSeqEdit, DNA92234 [Full], page 1

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                                                           scrFI[M.hpaII-]
                                                           nclI
                                                           mspI
                                                           hpaII                                          mnlI
                                                           dsaV                                         . bslI
                                             bpuAI  bsp1286                                       tsp45I
                                           bbsI bslI  bmyI                                  tru9I hphI
                               mnlI mboII bsaJI  bsmFI talI                                 mseI maeII
                          bbsI bslI  bsmFI talI  maeII/hpyCH4IV
           aluI.         mnlI mboII bsaJI

101 GATGTGAATA GCTCCACTAT ACCAGCCTCG TCTTCCTTCC GGGGGACAGC GTGGGTCAGG GCACAGAGAG ATATTTAATG TCACCCTCTT GGGGCTTTCA
    CTACACTTAT CGAGGTGATA TGGTCGGAGC AGAAGGAAGG CCCCCTGTCG CACCCAGTCC CGTGTCTCTC TATAAATTAC AGTGGGAGAA CCCCGAAAGT
                                                                                                              nLa

                                               sau3AI
                                               mboI/ndeII[dam-]
                                               dpnII[dam-]
                                               dpnI[dam+]
                                               alwI[dam-]
                                       nlaIV
                                       bstYI/xhoII                              hgaI
                      mnlI             bamHI bslI                               tseI
               rmaI                   alwI[dam-]  hpy188III            fnu4HI/bso
          mael       hpy188I bstXI    bslI  avaI    bhvI bsmFI
    bfaI   eco57I  bpmI/gsuI[dcm-]

    pleI
    mlyI
    hinfI
    bsmFI mnlI

201 TGGGACTCCC TCTGCCACAT TTTTTGGAGG TTGGGAAAGT TGCTAGAGGC TTCAGAACTC CAGCCTAATG GATCCCAAAC TCGGGAGAAT GGCTGCGTCC
    ACCCTGAGGG AGACGGTGTA AAAAACCTCC AACCCTTTCA ACGATCTCCG GTCGGATTAC CTAGGGTTTG AGCCCTCTTA CCGACGCAGG

  1                                       M   D   P   K   L   G   R . M   A   A   S
                                          ^MET
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GSeqEdit, DNA92234 [Full], page 2

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                                    fnu4HI/bsoFI
                              tseI  aclI
                        tseI  mwoI  thaI nlaIII
                  tseI  mwoI  fnu4HI/bsoFI  nspHI              haeII
            mwoI  fnu4HI/bsoFI  fnuDII/mvnI                    nspI
            fnu4HI/bsoFI        fnuDII/mvnI                    scrFI[M.hpaII-]
      bbvI  bbvI  bstUI[M.hhaI-]                               ncII
      tseI  tseI  bsh1236I                      dsaV hinPI     bpuAI                      ms
      mwoI  fnu4HI/bsoFI hinPI nspI       hphI  mwoI hpaII     bbsI:       rsaI           mnlI
mwoI  fnu4HI/bsoFI       hhaI/cfoI        mnlI  acII bssKI     xmnI mboII  csp6I          ecoNI
cacBI bbvI  bbvI  bpmI/gsuI[dcm-]   bseRI  mnlI bslI bsaJI hhaI/cfoI  asp700  bsrI        bslI

301 CTGCTGGCTG TGCTGCTGCT GCTGCTGGAG TCTCCTCGACC CTCCCGCCCC CCGGCGCTGT TAGAGAAAGT CTTCCAGTAC ATTGACCTCC
    GACGACCGAC ACGACGACGA CGACGACCTC AGAGGAGTGG GGGGGCGGGG GGCCGCGACA ATCTCTTTCA GAAGGTCATG TAACTGGAGG

12  L  A  V  L  L  L  L  E  R  G  M  F  S  S  P  S  P  P  P  A  L  L  E  K  V  F  Q  Y  I  D  L  H
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                                                                      mboII
                                                                      earI/ksp632I
                                                                      sapI
                                                                      aluI
                                                                      sstI
                                                                      sacI
                                            tth111I/aspI              hgIAI/aspHI[M.aluI-]
                                            pleI                      ecl136II
                          haeIII/pall       pflFI                     bspI286I[M.aluI-]
            alwNI[dcm-]    mscI/ball         nlyI                     bslHKAI hpy188I
  foki tsp509I  alw26I/bsmAI      eaeI  taqI  hinfI           hpy188I  bmyI eco57I        ea
  bstF5I     hpyCH4V                cfrI  hpy188III   mnlI eco57I     banII[M.aluI-]       cf
  hpy188III  bsgI hgaI eco57I

401 ATCAGGATGA ATTTGTGCAG AGCCTGAAGG AGTGGGTGGC CATCGAGAGC GACTCTGTCC AGCCTGTGCC TCGGTTCAGA CAAGAGCTCT TCAGAAATGAT
    TAGTCCTACT TAAACACGTC TCGGACTTCC TCACCCACCG GTAGCTCTCG CTGAGACAGG TCGGACACGG AGCCAAGTCT GTTCTCGAGA AGTCTTACTA

46  Q  D  E  F  V  Q  S  L  K  E  W  V  A  I  E  S  D  S  V  Q  P  V  P  R  F  R  Q  E  L  F  R  M  M
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GSeqEdit, DNA92234 [Full], page 3

```
                                                              tseI
                                                              fnu4HI/bsoFI
                                                              aluI
                                mwoI                          pvuII[M.H1-]
                                scrFI[dcm-]                   tseI
                                pspGI sau96I[M.haeIII-]        fnu4HI/bsoFI
                                mvaI pspOMI/bsp120I
                                ecoRII[dcm-]
                                dsaV[dcm-]
                                bstNI nlaIV
                                bssKI[dcm-]
                                hinPI bsp1286[M.haeIII-]
                                hhaI/cfoI sfiI
                                tseI bsaJI bmyI
                                fnu4HI/bsoFI sau96I[M.haeIII-]
                                bbvI apyI[dcm+]
                                                              sau96I alwNI[dcm-]              mboII
dsaI tseI       hpyCH4V      banII[M.haeIII-]                 ppuMI ddeI mspAlI/nspBII        bpuAI
btgI/betDSI     afcI haeII   apaI          mnlI               nlaIV bspCNI bbvI               bbsI
bsaJI  aclI     tseI alwNI[dcm-] haeIII/palI bsaJI            ecoO109I/draII                 pleI
mwoI fnu4HI/bsoFI pstI[M.H1-]  nlaIV        haeIII/palI       nlaIII mnlI bbvI               mlyI
bceAI bbvI      fnu4HI/bsoFI   ecoO109I/draII                 pshAI avaII alw26I/bsmAI        hinfI
haeIII/palI     bbvI alw26I/bsmAI bglII[M.haeIII-]                                     hpy188I    mnlI
501 GCCGGTGGCT GCGGACACGC TGCAGCGCCT GGGGGCCCGT GTGGCCTCGG TGGACATGGG TCCTCAGCAG CTGCCCGATG GTCAGAGTCT TCCAATACCT
    CGGCCACCGA CGCCTGTGCG ACGTCGCGGA CCCCCGGGCA CACCGGAGCC ACCTGTACCC AGGAGTCGTC GACGGGCTAC CAGTCTCAGA AGGTTATGGA
79 . A V A  A D T L Q R L  G A R V A S V  D M G  P Q Q  L P D G  Q S L  P I P
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eaeI[dcm-]
scrFII[dcm-]
pspGI
mvaI
ecoRII[dcm-]                                                                           scrFI[M.hpaII-]
dsaV[dcm-]              bslI         draIII                        tseI              nciI
bstNI bslI             sau3AI        mwoI          haeIII/palI     fnu4HI/bsoFI  mspI
bssKI[dcm-]            mboI/ndeII[dam-] bst4CI/hpyCH4III    bsgI  cac8I            hpaII
apyI[dcm+]             dpnII[dam-]   bstAPI        eaeI     talI bbvI              dsaV
foKI  cfrI  bsrI       dpnI[dam+]    nlaIV         cfrI     maeII/hpyCH4IV         bssKI
bstFSI haeIII/palI     alwI[dam-]    banI          mwoI  bceAI     btrI hpyCH4V    bsaJI
601 CCCGTCATCC TGGCCGAACT GGGGAGCGAT CCCACGGTGTG CTTCTACGGC CACTTGGACG TGCAGCCTGC TGACCGGGGC GATGGGTGGC
    GGGCAGTAGG ACCGGCTTGA CCCCTCGCTA GGGTGCTTTC CGTGGCACAC GAAGATGCCG AGTCGGACG ACTGGCCCCG CTACCCACCG
112  P  V  L    A  E  L   G  S  D    P  T  K  G   F  Y  G    H  L  D  V   Q  P  A   D  R  G   D  G  W   L
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                                                 sau3AI  mwoI
                                                 mboI/ndeII[dam-]          hl
                             bslI                dpnII[dam-]               hh
                             sau96I[M.haeIII-]   dpnI[dam+]
sau96I                       haeIII/palI         alwI[dam-]                hae
nlaIV         accI           ecoO109I/draII
avaII         mnlI    mnlI  mcrI
                      bseRI bslEI
701 TCACGGACCC CTATGTGCTG ACGGAGGTAG ACGGGAAACT TTATGGACGA GGAGGGACCG ACAACAAAGG CCCTGTCTTG GCTTGGATCA ATGCTGTGAG
    AGTGCCTGGG GATACACGAC TGCCCTCCATC TGCCCTTTGA AATACCTGCT CCTCGCTGGC TGTTGTTTCC GGGACAGAAC CGAACCTAGT TACGACACTC
146  T  D  P   Y  V  L    T  E  V  D   G  K  L  Y   G  R    G  A  T  D   N  K  G    P  V  L    A  W  I  N   A  V  S
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GSeqEdit, DNA92234 [Full], page 5

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                                                                        mnlI
scrFI[dcm-]                                                             bpmI/gsuI[dcm-]
pspGI                                                                   scrFI[dcm-]
mvaI    sau3AI                                                          pspGI
ecoRII[dcm-]                                                            mvaI
dsaV[dcm-] mboI/ndeII[dam-]                                             ecoRII[dcm-]
     bstNI    dpnII[dam-]                                               dsaV[dcm-]
bsp1286  bstYI/xhoII                                                    bstNI
  bmyI bssKI[dcm-] mboII                         foqI mboII cac8I       bssKI[dcm-]
  hpy188I apyI[dcm+] dpnI[dam+]                       bstF5I   mnlI     apyI[dcm+]
eco57I  bsaJI    bglII         tsp509I        mnlI    earI/ksp632I      bsaJI
mwoI banII bpmI/gsuI[dcm-]     apoI                                     

801 CGCCTTCAGA GCCCTGGAGC AAGATCTTCC ANATTCATCA TTGAGGGGAT GGAGGAGGCT GGCTCTGTTG CCCTGGAGGA ACTTGTGGAA
    GCGGAAGTCT CGGGACCTCG TTCTAGAAGG ACACTTATAG TTTAAGTAGT AACTCCCTA  CCTTCTCCGA CCGAGACAAC GGGACCTCCT TGAACACCTT
179 A  F  R  A  L  E  Q  D  L  P  V  N  I  K  F  I  I  E  G  M  E  E  A  G  S  V  A  L  E  E  L  V  E
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```
                                                                              sorFI(
                                                                              nciI
                                                                              mspI
                                                                              hpaII
                                                                              dsaV
                                                                              bssKI
                                                                              bsaJI
                                                                              xmaI/ps
                                                                              smaI
                                                                              scrFI[M
                                                                              nciI
                                                                              dsaV
                                                                              bssKI
                                                                              bsaJI
                                                                              avaI[M.
                                       sau3AI                                 nlaIV
                                       mboI/ndeII[dam-]
                                       dpnII[dam-]
                                       dpnI[dam+]
                    hpy188I            alwI[dam-]              cacBI
         tfII      tsp509I
  sau96I mboII
  avaII hinfI
901 AAGAAAAGG ACCGATTCTT CTCTGGTGTG GACTACACTTG TAATTTCAGA ATCAGCCAAA GGAAGCCAGC AATCACTTAT GGAACCCGGG
    TTNCTTTTCC TGGCTAAGAA GAGACCACAC CTGATGTAAC ATTAAAGTCT ATTGGACACC TAGTCGGTTT CCTTCGGTCG TTAGTGAATA CCTTGGGCCC
212 K  E  K  D  R  F  F  S  G  V  D  Y  I  V  I  S  D  N  L  W  I  S  Q  R  K  P  A  I  T  Y  G  T  R  G
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GSeqEdit, DNA92234 [Full], page 7

```
                                                         sau3AI        sap
                                                         mboI/ndeII[da
                                                         dpnII[dam-]
                                   nlaIII                dpnI[dam+] ea
                            fokI   rcaI
                            bstF5I hpy188III
                            afaNI  bspHI

scrFI[dcm-]
pspGI
mvaI
ecoRII[dcm-]
dsaV[dcm-]
bstNI
bssKI[dcm-]

               bsmAI  hpy188III
               bsaI   ddeI nlaIV
      hphI     hpyCH4V apyI[dcm+] bspCNI

aluI  nlaIII  mnlI

1001 GGAACAGCTA CTTCATGGTG GAGGTGAAAT GCAGAGACCA GGATTTCAC TCAGGAACCT TTGGTGGCAT CCTTCATGAA CCAATGGCTG ATCTGGTTGC
     CCTTGTCGAT GAAGTACCAC CTCCACTTTA CGTCTCTGGT CCTAAAAGTG AGTCCTTGGA AACCACCGTA GGAAGTACTT GGTTACCGAC TAGACCAACG
246  N  S  Y  E  V  K  C  R  D  Q  D  F  H  S  G  T  F  G  G  I  L  H  E  P  M  A  D  L  V  A
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                                                      scrFI[dcm-]
                                                      pspGI
                                                      mvaI
                                                      ecoRII[dcm-]
                                                      dsaV[dcm-]
                                                      bstNI
                                                      bssKI[dcm-]
                                                      sau96I[dcm-]
                                                      nlaIV
                             accI                     avaII[dcm-]
              scrFI[dcm-]    scrFI[dcm-]
              pspGI  pleI    pspGI  apyI[dcm+]
              mvaI   mlyI    mvaI  bsmFI
              ecoRII[dcm-]   ecoRII[dcm-]
              dsaV[dcm-]     dsaV[dcm-]
              bstNI  hinfI   bstNI  bsaJI                              mnlI
      mboII   bssKI[dcm-]    bssKI[dcm-] tfiI    xmnI  nlaIV  mboII
              apyI[dcm+]     apyI[dcm+]  hinfI   asp700 mnlI   earI/ksp632I

1101 TCTTCTCGGT AGCCTGGTAG ACTCGTCTGG TCATATCCTG GTCCCTGGAA TCTATGATGA AGTGGTTCCT CTTACAGAAG AGTGGTTCCT TACATACAAA
     AGAAGAGCCA TCGGACCATC TGAGCAGACC AGTATAGGAC CAGGGACCTT AGATACTACT TCACCAAGGA GAATGTCTTC TCCTTATTT ATGTATGTTT
279  L  L  G   S  L  V  D   S  S  G   H  I  L   V  P  G  I   Y  D  E   V  V  P   L  T  E  E   E  I  N   F  Y  K
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```
                                                          rsaI
                                          scrFI[M.hpaII-]  csp6I
                                            ndlI           nlaIV
                                            mspI           kpnI
                                            hpaII          banI
                                            dsaV           asp718
                                            bssKI          bpmI/gsuI[dcm
                rmaI                                       hpy188III
                maeI  rmaI                         mnlI tfII   mnlI  acc65I
                xbaI  maeI  mspI    tseI    fnu4HI/bsoFI  tsp509I   hpyCH4V  mnlI
          foHI hpy188III mboII  hpaII  bbvI    apoI  taqI ddeI bseRI hinEI
    bstF5I bfaI  bfaI  bsaWI
1201 GCCATCCATC TAGACCTAGA AGAATACCGG AATAGCAGCC GGGTTGAGGA ATTTCTGTTC GATACTAAGG AGGAGATTCT AATGGACCTC TGGAGGTACC
     CGGTAGGTAG ATCTGGATCT TCTTATGGCC TTATCGTCGG CCCAACTCTT TAAAGACAAG CTATGATTCC TCCTCTAAGA TTACGTGGAG ACCTCCATGG
312  A  I  H  L  D  L  E  B  Y  R  N  S  S  R  V  B  K  F  L  F  D  T  K  E  E  I  L  M  H  L  W  R  Y  P

                                          haeIII/palI
                                          eaeI[dcm-]
                                          cfrI
                     thaI           scrFI[dcm-]    scrFI[dcm-]
                     fnuDII/mvnI                   pspGI
                     hinPI          pspGI          mvaI
              mnlI bstUI[M.hhaI-]   mvaI
                     sau3AI  hhaI/cfoI   ecoRII[dcm-]   ecoRII[dcm-]
                     mboI/ndeII[dam-] [M.taqI-]         dsaV[dcm-]
                     dpnII[dam-]    dsaV[dcm-]    bstNI          tsp509I      bsm
                     dpnI[dam+]     bstNI         bssXI[dcm-]    apoI         rmaI
              alwI[dam-] bshl236I   bssKI[dcm-]   apyI[dcm+]     xmnI         maeI
              nlaIII  taqI[dam-]    apyI[dcm+]    bst4CI/hpyCH4III  asp700     bfaI
1301 CATCTCTTTC TATTCATGGG ATCGAGGGCG CGTTTGATGA GCCTGGAACT AAAACAGTCA TACCTGGCCG AGTTATAGGA AAATTTCAA TCCGTCTAGT
     GTAGAGAAAG ATAAGTACCC TAGCTCCCGC GCAAACTACT CGGACCTTGA TTTTGTCAGT ATGGACCGGC TCAATATCCT TTTAAAGTT AGGCAGATCA
346  S  L  S  I  H  G  I  E  G  A  P  D  E  P  G  T  K  T  V  I  P  G  R  V  I  G  K  F  S  I  R  L  V
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GSeqEdit, DNA92234 [Full], page 10

```
                                                              pl
                      nlaIII                                  nl
        msII        naeIII                                    hl
mnlI mslI  aclI    hphI    hpy188III   mboII      asp700  bstXI  nlaII
1401 CCCTCACATG AATGTGTCTG CGGTGGAAAA ACAGTGACA CGACATCTTG AAGATGTGTT CTCCAAAAGA AATAGTTCCA ACAAGATGGT TGTTTCCATG
     GGGAGTGTAC TTACACAGAC GCCACCTTTT TGTCCACTGT GCTGTAGAAC TTCTACACAA GAGGTTTTCT TTATCAAGGT TGTTCTACCA ACAAAGGTAC
379   P  H  M  N  V  S  A  V  B  K  Q  V  T  R  H  L  B  D  V  F  S  K  R  N  S  S  N  K  M  V  S  M

                                       tspRI
                              hpy188I                               sau
                       mwoI   sau3AI bst4CI/hpyCH4III              mbo
                       tseI    mboI/ndeII[dam-]                    dpn
     rmaI    dsaI          fnu4HI/bsoFI   dpnII[dam-]              dpn
     maeI    btgI/bstDSI sspI      bbvI   dpnI[dam+]               alw
     bfaI    bsaJI hpyCH4V   bsrI
1501 ACTTCTAGGAC TACACCCGTG GATTGCAAAT AATGATGACA CCCAGTATCT CGCCAGCAAA AGAGCGATCA GAACAGTGTT TGGAACAGAA CCAGATATGA
     TGAGATCCTG ATGTGGGCAC CTAACGTTTA TAACTACTGT GGGTCGTTAGA TCTCGCTAGT CTTGTCACAA ACCTTGTCTT GGTCTATACT
412   T  L  G  L  H  P  W  I  A  N  I  D  D  T  Q  Y  L  A  A  K  R  A  I  R  T  V  F  G  T  E  P  D  M  I
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                                                                                                    tru9I
                                                                                              aluI  mseI
sau3AI                                                             tseI                  sau96I[M.haeIII-]
  mboI/ndeII[dam-]                    serFI[dcm-]                    fnu4HI/bsoFI            haeIII/palI aseI/asnI/vspI
    dpnII[dam-]                 sau3AI  pspGI  mboI/ndeII[dam-]                    ddeI
  foxI dpnI[dam+]                       nvaI   dpnII[dam-]           nlaIV  tsp509I bbvI
    bstF5I                                ecoRII[dcm-]                   mnlI
    sccFI[M.hpaII-]                       dsaV[dcm-]
  nciI  alwI[dam-]                      bstNI  dpnI[dam+]
  mspI  nlaIV                             bssKI[dcm-]
  hpaII bstYI/xhoII                       apyI[dcm+]         mwoI  aciI. aluI
  dsaV  bamHI            tsp509I                       tsp509I
  bssKI alwI[dam-]       munI/mfeI                mspAlI/nspBII
1601 TCCGGGATGG ATCCACCATT CCAATTGCCA AAAGTTCCA GGAGATCGTC CACAAGAGCG TGGTGCTAAT TCCGCTGGGA GCTGTTGATG ATGGAGAACA
     AGGCCCTACC TAGGTGGTAA GGTTAACGGT TTTACAAGGT CCCTAGCAG GTGTTCTCGC ACCACGATTA AGGCGACCCT CGACAACTAC TACCTCTTGT
446   R  D  G   S  T  I   P  I  A  K   M  F  Q   E  I  V  H   K  S  V   V  L  I  P   L  G  A  V   D  D  G  E   E

1701 TTCGCAGAAT GAGAAAATCA ACAGGTGGAA CTACATAGAG GGAACCAAAT TATTGCTGC CTTTTTCTTA GAGATGGCCC AGCTCCATTA ATCACAGAA
     AAGCGTCTTA CTCTTTTAGT TGTCCACCTT GATGTATCTC CCTTGGTTTA ATAAACGACG GAAAAAGAAT CTCTACCGGG TCGAGGTAAT TAGTGTCTT
479   S  Q  N   E  K  I  N   R  W  N   Y  I  E   G  T  K  L   F  A  A   F  F  L  E   M  A  Q   L  H  O
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sau3AI
mboI/ndeII[dam-]
dpnII[dam-]
dpnI[dam+]
hpy188I   rmaI
          sau3AI   tspRI   maeI
     hpy188I alwI[dam-]   bslI
rmaI   mboI/ndeII[dam-]   hphI   bslI   tsp509I   rmaI
maeI   dpnII[dam-]   tfiI   mnlI   fokI bfaI   fokI   apoI maeI rsaI
bfaI   dpnI[dam+]   hinfI[M.hphI-]   bstF9I   bstF5I   hpy188III   bfaI csp6I

1801 CCTTCTAGTC TGATCTGATC CACTGACAGA TTCACCTCCC CCACATCCCT AGACAGGGAT GGAATGTAAA TATCCAGAGA ATTTGGGTCT AGTATAGTAC
     GGAAGATCAG ACTAGACTAG GTGACTGTCT AAGTGGAGGG GGTGTAGGGA TCTGTCCCTA CCTTACATTT ATAGGTCTCT TAAACCCAGA TCATATCATG

                                                                                       sau96I
                          sau3AI   nlaIV
                          mboI/ndeII[dam-]   avaII   hpyCH4V
                          dpnII[dam+]   ppuMI   bsgI
          tru9I   dpnI[dam+]   eco0109I/draII
          mseI   hpy188III   tru9I   tspRI
     ahaIII/draI   ecoRV   alwI[dam-]   sspI   mseI bsmFI btsI

1901 ATTTTCCCTT CCATTTAAAA TGTCTTGGGA TATCCTGGATC AGTAATAAAA TATTTCAAAG GCACAGAGTGT TGGAAATGGT TTAAGGTCCC CCACTGCACA
     TAAAAGGGAA GGTAAATTTT ACAGAACCCT ATAGACCTAG TCATTATTTT ATAAAGTTTC CGTGTCTACA ACCTTTACCA AATTCCAGGG GGTGACGTGT

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```
                                                            scrFI[dcm-]
                                                            pspGI
                                                            mvaI
                                                            ecoRII[dcm-]
                                                            dsaV[dcm-]
                                                            bstNI
                                                            bssKI[dcm-]
                                                            apyI[dcm+]
                                                            bslI    tfiI
                                                            hpyCH4V bsaJI  hinfI
                          tseI
                 cac8I
                       tseI    fnu4HI/bsoFI
                       fnu4HI/bsoFI
        smlI     bbvI   bbvI
        mnlI     aluI   hpyCH4V
   2001 CCTTCCTCAA GTCATAGCTG CTTGCAGCAA CTTGATTCC CCAAGTCCTG TGCAATAGCC CCAGGATTGG ATTCCTTCCA ACCTTTAGC ATATCTCCAA
        GGAAGGAGTT CAGTATCGAC GAACGTCGTT GAACTAAAGG GGTTCAGGAC ACGTTATCGG GGTCCTAACC TAAGGAAGGT TGGAAAATCG TATAGAGGTT

                                          sau96I            tsp45I
                                          avaII    bssSI
                                          ppuMI    hg1AI/aspHI
                                          eco01091/draII hpyl88III
                              mspI    rmaI    bsp1286
                              hpaII   maeI   smlI   bslHKAI
                              bsaWI   bfaI   mnlI   bmyI  maeIII
           tsp509I                                        fokI
           hpyCH4V                                        bstF5I
   2101 CCTTGCAATT TGAATTGGCAT AATCACTCCG GTTTGCTTTC TAGGTCCTCA AGTGGTCGTG ACACATAATC ATTCCATCCA ATGATCGCCT TTGCTTTACC
        GGAACGTTAA ACTAACCGTA TTAGTGAGGC CAAACGAAAG ATCCAGGAGT TCACGAGCAC TGTGTATTAG TAAGGTAGGT TACTAGCGGA AACGAAATGG

              tru9I         bsmAI
              mseI          bsaI
              aseI/asnI/vspI         tspRI
   2201 ACTCTTTCCT TTTATCTTAT TAATAAAAT GTTGGTCTCC ACCACTGNCT CCCAAAAAAA AAAAAAAAAA AAGAAAAAAA AAAAAAAAAA AAAAAAAAAA
        TGAGAAAGGA AAATAGAATA ATTATTTTTA CAACCAGAGG TGGTGACNGA GGGTTTTTTT TTTTTTTTTT TTCTTTTTTT TTTTTTTTTT TTTTTTTTTT

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                                                    scrFI[M.hpaII-]
                                                    nciI
                                                    mspI
                                                    hpaII
                                                    dsaV
                                                    bssKI           sau96I rsaI
                                                    xmaI/pspAI      rsrII/cspI
                                                    smaI      mroI  nlaIV
                              acII                  scrFI[M.hpaII-] cpoI  kpnI  hpyCH4V
           fnu4HI/bsoFI       taqI ncII            hpy188III csp6I
           haeIII/palI   sstI salI dsaV            bspMII  banI sfcI
           mcrI          sacI hincII/hindII[M.taqI-] avaII[M.hpaII-]
           eagI/xmaIII/eclXI aluI accII[M.taqI-] tru9I mspI       asp718
           eaeI          hgiAI/aspHI[M.aluI-] mseI bspEI cfr10I/bsrFI
           cfrI    xmaI  ecl136II  bssKI  aseI/asnI/vspI  acc65I  cac8I
           bslEI   maeI  bspi286[M.aluI-] xmnI tsp509I bsaWI  pstI
           notI    bfaI  bslBKAI  bsaJI tsp509I bsaWI ageI  sse8387I
           fnu4HI/bsoFI  bmyI hpy99I avaI[M.hpaII-] hpaII mspI bspMI     rsaI
           acII    speI  banII[M.aluI-]  asp700  accIII hpaII sbfI  csp6I aluI   sf

2301 AAAAAAAAAA AAAAAAAAAA AAAGGGCGGC CGCCGACTAG TGAGCTCGTC GACCCGGGAA TTAATTCCGG ACCGGACCT GCAGGCGTAC CAGCTTCCC
     TTTTTTTTTT TTTTTTTTTT TTTCCCGCCG GCGGCTGATC ACTCGAGCAG CTGGGCCCTT AATTAAGGCC TGGCCATGGA CGTCCGCATG GTCGAAAGGG

           pleI
           mlyI
           hinfI   aluI

2401 TATAGTGAGT CGTATTAGAG CTTGG
     ATATCACTCA GCATAATCTC GAACC
```

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> length: 2425

aatII (GACGTC):   25
acc65I (GGTACC):   1295 2374
accI (GTMKAC):   727 1117 2348
accIII (TCCGGA):   2366
aclI (CCGC):   86 332 355 511 1420 1672 2326 2330
acyI (GRCGYC):   25
aflIII (ACRYGT):   37
ageI (ACCGGT):   2371
ahaII (GRCGYC):   25
ahaIII (TTTAAA):   1914
aluI (AGCT):   19 48 110 485 569 1006 1680 1781 2016 2343 2392 2419
alw26I (CAGNNNCTG):   418 523 565
alwI (GGATCNNNN):   270 271 628 785 959 1319 1599 1609 1610 1817 1936
alwNI (CAGNNNCTG):   418 523 565
apaI (GGGCCC):   533
apoI (RAATTY):   54 409 841 1249 1381 1879
apyI (CCWGG):   528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
aseI (ATTAAT):   1787 2219 2360
asnI (ATTAAT):   1787 2219 2360
asp700 (GAANNNNTTC):   375 1159 1379 1469 2358
asp718 (GGTACC):   1295 2374
aspHI (GWGCWC):   484 2152 2342
aspI (GACNNNGTC):   451
avaI (CYCGRG):   62 280 995 2353
avaII (GGWCC):   559 705 909 1140 1985 2143 2369
balI (TGGCCA):   437
bamHI (GGATCC):   270 1609
banI (GGYRCC):   640 1295 2374

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banII (GRGCYC) :   484 533 809 2342
bbsI (GAAGACNNNNNN) :   130 379 587
bbvI (GCAGC) :   292 312 315 318 321 508 519 522 567 570 672 1235 1552 1756 2017 2024
bceAI (ACGGCNNNNNNNNNNNN) :   502 656
bfaI (CTAG) :   243 1210 1216 1396 1504 1805 1849 1889 2140 2337
bglI (GCCNNNNNGGC) :   535
bglII (AGATCT) :   822
bmyI (GDGCHC) :   159 484 533 809 2152 2342
bpmI (CTGGAG) :   96 258 325 814 883 1290
bpuAI (GAAGACNNNNNN) :   130 379 587
bsaAI (YACGTR) :   42
bsaHI (GRCGYC) :   25
bsaI (GGTCTCNNNNN) :   1034 2234
bsaJI (CCNNGG) :   139 359 503 528 545 684 812 881 995 996 1143 1516 2060 2353
bsaWI (WCCGGW) :   1226 2127 2366 2371
bseRI (GAGGAGNNNNNNNNNN) :   342 749 1270
bsgI (GTGCAG) :   415 670 1994
bsh1236I (CGCG) :   38 331 1329
bsiEI (CGRYCG) :   755 2327
bsiHKAI (GWGCWC) :   484 2152 2342
bsiWI (CGTACG) :   40
bslI (CCNNNNNNNGG) :   135 184 274 275 354 396 614 631 771 1847 1898 2060
bsmAI (GTCTC) :   1034 2235
bsmAI (GTCTC) :   1034 2235
bsmFI (GGGACNNNNNNNNNNNNNN) :   143 202 297 1141 1399 1986
bsoFI (GCNGC) :   85 292 312 315 318 321 332 508 519 522 567 570 672 1235 1552 1756
                                               2017 2024 2326 2329
bsp120I (GGGCCC) :   533
bsp1286I (GDGCHC) :   159 484 533 809 2152 2342
bspCNI (CTCAGNNNNNNNNN) :   563 1050

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bspEI(TCCGGA):      2366
bspHI(TCATGA):      1074
bspMI(ACCTGC):      2377
bspMII(TCCGGA):     2366
bsrFI(RCCGGY):      2371
bsrI(ACTGGN):       384 618 1542
bssKI(CCNGG):       139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
                    1363 1602 1638 2061 2353 2354
bssSI(CTCGTG):      2155
bst4CI(ACNGT):      643 1354 1573
bstAPI(GCANNNNNTGC): 641
bstDSI(CCRYGG):     503 1516
bstFSI(GGATG):      405 606 857 1068 1203 1605 1844 1857 2175
bstNI(CCWGG):       528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
bstUI(CGCG):        38 331 1329
bstXI(CCANNNNNNTGG): 260 1478
bstYI(RGATCY):      270 822 1609
btgI(CCRYGG):       503 1516
btrI(CACGTC):       667
btsI(GCAGTGNN):     1992
cac8I(GCNNGC):      31 35 303 675 868 975 2020 2381
cfoI(GCGC):         330 364 525 800 1328
cfr10I(RCCGGY):     2371
cfrI(YGGCCR):       437 500 611 657 1365 2327
cpoI(CGGWCCG):      2368
csp6I(GTAC):        41 387 1296 1897 2375 2387
cspI(CGGWCCG):      2368
ddeI(CTNAG):        563 1050 1265 1767
dpnI(GATC):         271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
                    2183
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dpnII (GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
              2183

draI (TTTAAA): 1914

draII (RGGNCCY): 532 558 768 1984 2142

draIII (CACNNNGTG): 642

dsaI (CCRYGG): 503 1516

dsaV (CCNGG): 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
              1363 1602 1638 2061 2353 2354

eaeI (YGGCCR): 437 500 611 657 1365 2327

eagI (CGGCCG): 2327

earI (CTCTTCNNNN): 15 487 862 1100 1177

ecl136II (GAGCTC): 484 2342

eclXI (CGGCCG): 2327

eco57I (CTGAAG): 250 424 474 489 804

ecoNI (CCTNNNNNAGG): 396

ecoO109I (RGGNCCY): 532 558 768 1984 2142

ecoRI (GAATTC): 54

ecoRII (CCWGG): 528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061

ecoRV (GATATC): 1929

fnu4HI (GCNGC): 85 292 312 315 318 321 332 508 519 522 567 570 672 1235 1552 1756
                2017 2024 2326 2329

fnuDII (CGCG): 38 331 1329

fokI (GGATG): 405 606 857 1068 1203 1605 1844 1857 2175

gsuI (CTGGAG): 96 258 325 814 883 1290

haeII (RGCGCY): 363 524 799

haeIII (GGCC): 438 501 534 543 612 658 769 1366 1776 2328

hgaI (GACGC): 295 420

hgiAI (GWGCWC): 484 2152 2342

hhaI (GCGC): 330 364 525 800 1328

hinPI (GCGC): 330 364 525 800 1328

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hincII(GTYRAC): 2348
hindII(GTYRAC): 2348
hinEI(GANTC): 204 451 585 914 1120 1148 1275 1500 1829 2070 2407
hinlI(GRCGYC): 25
hpaII(CCGG): 139 361 684 996 1227 1239 1602 2128 2354 2367 2372
hphI(GGTGA): 3 181 346 1023 1434 1832
hpy188I(TCNGA): 51 79 252 476 491 582 806 946 1568 1809 1814
hpy188III(TCNNGA): 97 281 402 443 1051 1074 1209 1289 1446 1873 1933 2156 2366
hpy99I(CGWCG): 27 2347
hpyCH4III(ACNGT): 643 1354 1573
hpyCH4IV(ACGT): 26 43 149 668
hpyCH4V(TGCA): 34 416 521 671 1030 1283 1524 1995 2023 2051 2104 2380
kpnI(GGTACC): 1295 2374
ksp632I(CTCTTCNNNNN): 15 487 862 1100 1177
maeI(CTAG): 243 1210 1216 1396 1504 1805 1849 1889 2140 2337
maeII(ACGT): 26 43 149 668
maeIII(GTNAC): 4 180 1435 2158
mboI(GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937 2183
mboII(GAAGA): 15 131 380 488 588 825 862 917 1101 1177 1219 1450
mcrI(CGRYCG): 755 2327
mfeI(CAATTG): 1622
mluI(ACGCGT): 37
mlyI(GAGTCNNNNN): 204 451 585 1120 1500 2407
mnlI(CCTC): 65 77 126 185 209 227 246 344 350 396 469 545 562 598 724 749 853 865 886 1021 1168 1180 1270 1287 1293 1324 1402 1738 1835 2005 2146 2366
mroI(TCCGGA): 437
mscI(TGGCCA): 175 1788 1915 1981 2220 2361
mseI(TTAA): 400 1405 1407
mslI(CAYNNNNRTG):

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mspAII(CMGCKG):     568 1672
mspI(CCGG):         139 361 684 996 1227 1239 1602 2128 2354 2367 2372
munI(CAATTG):       1622
mvaI(CCWGG):        528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
mvnI(CGCG):         38 331 1329
mwoI(GCNNNNNNNGC):  303 312 315 321 357 502 535 641 650 793 802 1555 1665
ncII(CCSGG):        139 360 684 995 996 1239 1602 2353 2354
ndeII(GATC):        271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
                    2183
nlaIII(CATG):       32 199 336 555 1014 1075 1315 1407 1497
nlaIV(GGNNCC):      270 532 533 558 640 705 991 1054 1140 1164 1295 1609 1741 1985 2374
notI(GCGGCCGC):     2326
nspBII(CMGCKG):     568 1672
nspHI(RCATGY):      31 335
nspI(RCATGY):       31 335
paeR7I(CTCGAG):     62
palI(GGCC):         438 501 534 543 612 658 769 1366 1776 2328
pflPI(GACNNNGTC):   451
pleI(GAGTCNNNN):    204 451 585 1120 1500 2407
ppuMI(RGGWCCY):     558 1984 2142
pshAI(GACNNNNGTC):  553
pspAI(CCCGGG):      995 2353
pspGI(CCWGG):       528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
pspOMI(GGGCCC):     533
pstI(CTGCAG):       520 2379
pvuII(CAGCTG):      568
rcaI(TCATGA):       1074
rmaI(CTAG):         243 1210 1216 1396 1504 1805 1849 1889 2140 2337
rsaI(GTAC):         41 387 1296 1897 2375 2387
rsrII(CGGWCCG):     2368
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sacI (GAGCTC): 484 2342
salI (GTCGAC): 2348
sapI (GCTCTTCNNNN): 15 486 1099
sau3AI (GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937 2183
sau96I (GGNCC): 533 534 559 705 769 909 1140 1776 1985 2143 2369
sbfI (CCTGCAGG): 2378
scrFI (CCNGG): 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342 1363 1602 1638 2061 2353 2354
sfaNI (GCATC): 1067
sfcI (CTRYAG): 10 520 2379 2400
sfiI (GGCCNNNNNGGCC): 534
smaI (CCCGGG): 995 2353
smlI (CTYRAG): 62 2006 2147
snaBI (TACGTA): 42
speI (ACTAGT): 2336
sphI (GCATGC): 31
splI (CGTACG): 40
sse8387I (CCTGCAGG): 2378
sspI (AATATT): 1528 1949
sstI (GAGCTC): 484 2342
taiI (ACGT): 26 43 149 668
taqI (TCGA): 63 443 1259 1322 2349
tfiI (GAWTC): 914 1148 1275 1829 2070
thaI (CGCG): 38 331 1329
tliI (CTCGAG): 62
trp9I (TTAA): 175 1788 1915 1981 2220 2361
tseI (GCWGC): 292 312 315 318 321 508 519 522 567 570 672 1235 1552 1756 2017 2024
tsp45I (GTSAC): 4 180 1435 2158
tsp509I (AATT): 55 410 842 942 1250 1382 1623 1668 1748 1880 2107 2359 2363

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tspRI (NNCAGTGNN):   1574 1821 1992 2243
tth111I (GACNNNGTC):   451
vspI (ATTAAT):   1787 2219 2360
xbaI (TCTAGA):   1209
xhoI (CTCGAG):   62
xhoII (RGATCY):   270 822 1609
xmaI (CCCGGG):   995 2353
xmaIII (CGGCCG):   2327
xmnI (GAANNNNTTC):   375 1159 1379 1469 2358

not found:
aclI (AACGTT), afeI (AGCGCT), aflII (CTTAAG), ahdI (GACNNNNNGTC), alw44I (GTGCAC), apaLI (GTGCAC), ascI (GGCGCGCC),
avaIII (ATGCAT), avrII (CCTAGG), baeI (NNNNNNNNNNNNNNNNACNNNNGTAYCNNNNNNNNNNNN), bbrPI (CACGTG),
bcgI (NNNNNNNNNNCGANNNNNNTGCNNNNNNNNNN), bclVI (GTATCC), bclI (TGATCA), bfrBI (ATGCAT), bfrI (CTTAAG), blnI (CCTAGG),
blpI (GCTNAGC), bpu1102I (GCTNAGC), bsaBI (GATNNNNATC), bsaXI (NNNNNNNNNNNNACNNNNNCTCCNNNNNNNNNN), bsiCI (TTCGAA),
bsmBI (CGTCTCNNNN), bsmI (GAATGCN), bsp106 (ATCGAT), bsp1407I (TGTACA), bspCI (CGATCG), bspDI (ATCGAT), bsrBI (GAGCGG),
bsrDI (GCAATGNN), bsrGI (TGTACA), bssHII (GCGCGC), bst1107I (GTATAC), bstBI (TTCGAA), bstEII (GGTNACC), bstZ17I (GTATAC),
bsu36I (CCTNAGG), celII (GCTNAGC), claI (ATCGAT), drdI (GACNNNNNNGTC), eam1105I (GACNNNNNGTC), eclI (GGCGGA), eco47III (AGCGCT),
eco72I (CACGTG), eco81I (CCTNAGG), eheI (GGCGCC), espI (GCTNAGC), esp3I (CGTCTC), fseI (GGCCGGCC), fspI (TGCGCA), hindIII (AAGCTT),
hpaI (GTTAAC), kasI (GGCGCC), kspI (CCGCGG), manI (GATNNNNATC), mstII (CCTNAGG), naeI (GCCGGC), narI (GGCGCC), ncoI (CCATGG),
ndeI (CATATG), ngoMI (GCCGGC), nheI (GCTAGC), nruI (TCGCGA), nsiI (ATGCAT), pacI (TTAATTAA), pciI (ACATGT), pflMI (CCANNNNNTGG),
pmeI (GTTTAAAC), pmlI (CACGTG), ppu10I (ATGCAT), psiI (TTATAA), psp1406I (AACGTT), pvuI (CGATCG), sacII (CCGCGG), sanDI (GGGWCCC),
sauI (CCTNAGG), scaI (AGTACT), sceI (TAGGGATAACAGGGTAAT), sexAI (ACCWGGT), sfuI (TTCGAA), sgfI (GCGATCGC), sgrAI (CRCCGGYG),
snoI (GTGCAC), srfI (GCCCGGGC), sstII (CCGCGG), stuI (AGGCCT), styI (CCWWGG), swaI (ATTTAAAT),
xcmI (CCANNNNNNNNNTGG)

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